OM protein - protein search, using sw model

Run on: December 18, 2007, 01:07:39 ; Search time 507 Seconds
(without alignments)
122.510 Million cell updates/sec

Title: US-10-551-550-2
Perfect score: 2375
Sequence: 1 MAAHLLPICALFLTLLDMAQ.....FKCRCYPGWQAPWCERKSMW 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS2/ptodata/1/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS2/ptodata/1/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS2/ptodata/1/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS2/ptodata/1/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS2/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS2/ptodata/1/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS2/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2375	100.0	435	2	US-08-987-743-6	Sequence 6, Appli
2	2364	99.5	435	2	US-08-733-360A-1	Sequence 1, Appli
3	2364	99.5	435	2	US-08-916-935-1	Sequence 1, Appli
4	2364	99.5	435	3	US-10-622-283-1	Sequence 1, Appli
5	2364	99.5	435	3	US-09-795-914A-1	Sequence 1, Appli
6	2361	99.4	435	2	US-08-733-360A-3	Sequence 3, Appli
7	2361	99.4	435	2	US-08-987-743-15	Sequence 15, Appl
8	2361	99.4	435	2	US-08-916-935-3	Sequence 3, Appli
9	2361	99.4	435	3	US-10-622-283-3	Sequence 3, Appli
10	2361	99.4	435	3	US-09-795-914A-3	Sequence 3, Appli
11	1760	74.1	449	2	US-08-987-743-7	Sequence 7, Appli
12	1691	71.2	311	2	US-08-987-743-2	Sequence 2, Appli
13	898.5	37.8	481	2	US-09-949-016-6826	Sequence 6826, Ap
14	898.5	37.8	486	2	US-09-949-016-8176	Sequence 8176, Ap
15	879.5	37.0	529	1	US-07-779-890-2	Sequence 2, Appli

16	879.5	37.0	529	1	US-07-779-890-2	Sequence 2, Appli
17	879.5	37.0	529	5	PCT-US93-05640-2	Sequence 2, Appli
18	839.5	35.3	509	1	US-07-779-890-6	Sequence 6, Appli
19	839.5	35.3	509	1	US-07-779-890-6	Sequence 6, Appli
20	839.5	35.3	509	5	PCT-US93-05640-6	Sequence 6, Appli
21	839.5	35.3	514	2	US-09-949-016-9979	Sequence 9979, Ap
22	831.5	35.0	509	1	US-09-008-962-3	Sequence 3, Appli
23	831.5	35.0	509	1	US-08-675-507-3	Sequence 3, Appli
24	831.5	35.0	509	2	US-09-213-205-3	Sequence 3, Appli
25	831.5	35.0	509	2	US-08-733-360A-10	Sequence 10, Appl
26	831.5	35.0	509	2	US-08-916-935-11	Sequence 11, Appl
27	831.5	35.0	509	3	US-10-622-283-11	Sequence 11, Appl
28	831.5	35.0	509	3	US-09-795-914A-11	Sequence 11, Appl
29	829.5	34.9	474	2	US-10-360-101-242	Sequence 242, App
30	797	33.6	512	1	US-07-779-890-4	Sequence 4, Appli
31	797	33.6	512	1	US-07-779-890-4	Sequence 4, Appli
32	797	33.6	512	1	US-09-008-962-4	Sequence 4, Appli
33	797	33.6	512	1	US-08-675-507-4	Sequence 4, Appli
34	797	33.6	512	2	US-09-213-205-4	Sequence 4, Appli
35	797	33.6	512	5	PCT-US93-05640-4	Sequence 4, Appli
36	787	33.1	344	1	US-08-180-209B-58	Sequence 58, Appl
37	787	33.1	344	2	US-08-474-853-58	Sequence 58, Appl
38	787	33.1	344	2	US-09-166-205B-58	Sequence 58, Appl
39	787	33.1	344	5	PCT-US94-02629-58	Sequence 58, Appl
40	749.5	31.6	434	1	US-09-008-962-1	Sequence 1, Appli
41	749.5	31.6	434	1	US-08-675-507-1	Sequence 1, Appli
42	749.5	31.6	434	2	US-09-213-205-1	Sequence 1, Appli
43	749.5	31.6	434	2	US-10-222-032-2	Sequence 2, Appli
44	582	24.5	311	2	US-10-104-047-3429	Sequence 3429, Ap
45	529	22.3	102	2	US-08-987-743-9	Sequence 9, Appli

ALIGNMENTS

```
RESULT 1
US-08-987-743-6
; Sequence 6, Application US/08987743
; Patent No. 6123938
; GENERAL INFORMATION:
;  APPLICANT: Stern, Robert
;  APPLICANT: Csoka, Anthony
;  APPLICANT: Frost, Gregory I.
;  APPLICANT: Wong, Tim M.
;  TITLE OF INVENTION: Purification and Microsequencing of
;  TITLE OF INVENTION: Hylauronidase Isozymes
;  FILE REFERENCE: 9076/088CIP2
;  CURRENT APPLICATION NUMBER: US/08/987,743
;  CURRENT FILING DATE: 1997-12-09
;  EARLIER APPLICATION NUMBER: 08/733,360
;  EARLIER FILING DATE: 1996-10-17
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 435
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-08-987-743-6

  Query Match             100.0%;  Score 2375;  DB 2;  Length 435;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-227;
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  Matches  435;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAHLLPICALFLTLLDMAQGFRGPLLPNRPFTTVWNANTQWCLERHGVDVDVSVFDVVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAHLLPICALFLTLLDMAQGFRGPLLPNRPFTTVWNANTQWCLERHGVDVDVSVFDVVA 60

Qy         61 NPGQTFRGPDMTIFYSSQLGTYPYYTPTGEPVFGGLPQNASLIAHLARTFQDILAAIPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NPGQTFRGPDMTIFYSSQLGTYPYYTPTGEPVFGGLPQNASLIAHLARTFQDILAAIPAP 120

Qy        121 DFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAAR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAAR 180

Qy        181 AWMAGTLQLGRALRPRGLWGFYGFPDCYNYDFLSPNYTGQCPSGIRAQNDQLGWLWGQSR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AWMAGTLQLGRALRPRGLWGFYGFPDCYNYDFLSPNYTGQCPSGIRAQNDQLGWLWGQSR 240

Qy        241 ALYPSIYMPAVLEGTGKSQMYVQHRVAEAFRVAVAAGDPNLPVLPYVQIFYDTTNHFLPL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ALYPSIYMPAVLEGTGKSQMYVQHRVAEAFRVAVAAGDPNLPVLPYVQIFYDTTNHFLPL 300

Qy        301 DELEHSLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQ 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DELEHSLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQ 360

Qy        361 ALCSGHGRCVRRTSHPKALLLLNPASFSIQLTPGGGPLSLRGALSLEDQAQMAVEFKCRC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ALCSGHGRCVRRTSHPKALLLLNPASFSIQLTPGGGPLSLRGALSLEDQAQMAVEFKCRC 420

Qy        421 YPGWQAPWCERKSMW 435
              |||||||||||||||
Db        421 YPGWQAPWCERKSMW 435

<!--EndFragment-->
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